Estimates of Additive and Dominance Genetic Effects for Sow Longevity

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Summary and Implications

The purpose of current study was to estimate variance components, especially dominance genetic variation, for overall leg action, length of productive life, and sow stayability until third and fifth parity. This project evaluated the data from Finnish litter recording scheme. The variance components were estimated in two purebred (Landrace, n=23,602 and Large White, n=22,984) and crossbred (Landrace x Large White, n=17,440) datasets. The fixed effect of herd-year, and random effects of additive sire, parental dominance, and litter were included in the statistical model of all the traits. Moreover, the fixed effect of breeding consultant, and linear regression of test weight were also included in the statistical model for overall leg action. The estimated heritabilities of these traits ranged between 0.04 and 0.06, and were very similar between the different breeds. Similarly, the estimates for ratio of dominance variance to phenotypic variance ($d^2$) varied between 0.01 and 0.17, the highest from the crossbred dataset. Moreover, all the $d^2$ estimates in crossbred population were higher than the corresponding heritability estimates. However, in purebred populations, $d^2$ estimates were generally lower than the corresponding $h^2$ estimates. All the genetic correlations between same traits from purebred and crossbred were high. This indicates that the genetic gain in purebred populations will be passed on to the commercial crossbred sows. Based on current results, we suggest considering accounting for the effect of dominance in the breeding value estimation of sow longevity, especially when data from crossbred animals are included. Moreover, because dominance genetic variation for sow longevity exists, it should be possible to use that variation by planning the mating pairs to produce sows for commercial production.

Introduction

In general, the objective of breeding program is to improve genetic material of animals utilized in commercial production. In modern pork production units, the production is based on crossbred Landrace x Large White sows. Thus, the breeding objective in Landrace and Large White populations is to improve efficiency of crossbred sows, and their offspring.

Genetic gain of crossbred progeny through selection in purebred populations is dependent on the genetic correlation between same trait of purebred and crossbred population (Bijma et al., 2001). If that correlation is low, genetic gain in “purebred traits” is not realized in crossbred production. In that case, selection should be based on information collected from crossbred sows and their progeny. When the correlation appears to be lower than one, it is likely the result of genetic x environment interaction and non-additive (e.g. dominance) genetic effects. The correlation estimates between “same” trait in purebred and crossbred populations has varied between traits and populations studied. For example, Lutaaya et al. (2001) estimated genetic correlations of daily gain and backfat thickness between purebred (A, B) and their reciprocal cross (C) populations. They found daily gain was closely (0.99) correlated between A and C, whereas the corresponding correlation between B and C was only 0.62. Both the backfat correlations were clearly lower than one (A-C: 0.32, B-C: 0.70).

As sow longevity is considered as a ‘fitness trait’, it may be assumed to be affected highly by crossbreeding and non-additive genetic effects (Falconer and Mackay, 1996). The knowledge about genetic correlation between sow longevity in crossbred and purebred sows, and dominance genetic variation is needed in optimization of breeding program and breeding value estimation for sow longevity. Thus, the objective of this study was to estimate these parameters and to discuss the proper way to utilize crossbred vs. purebred information in breeding value estimation.

Materials and Methods

Data from Finnish litter recording scheme was utilized to estimate dominance genetic variation, and additive genetic correlations between “same” longevity related traits (stayability until 3rd and 5th parities, length of productive life and overall leg action) of crossbred and purebred populations. Stayabilities were recorded as a binary trait, i.e., whether sow has reached the parity (3 or 5) or not. Length of productive life was recorded as an interval from first farrowing to culling or death of sow. Overall leg action was scored with the scale from one to five by a breeding advisor. Records were utilized only from largest farms and it contained information on 23,602 Landrace, 22,984 Large White, and 17,440 Crossbred sows.

To study how “same traits” in purebred (LR, LW) and crossbred (LR x LW) populations are genetically correlated, the same trait in different populations were treated as different traits in three trait model. Five different analyses were carried out for all the traits to compare the effect of accounting sows inbreeding (F), sows common litter environment (L), and parental dominance (D) in the statistical model on these correlations. In all the models, fixed effect of farm and year interaction and random additive genetic effect of sire were included for all the traits. Similarly, the fixed effect of scorer (farm advisor) and fixed regression of on-farm test weight was included in the
statistical models of overall leg action in all the analyses. In
matrix notation, the most complicated statistical model for
records of crossbred sows can be written as:
\[ y = Xb + Z_{LR}u_{LR} + Z_{LW}u_{LW} + Wl + Hd + e, \]
where \( b \) is the vector of fixed effects, \( u_{LR} \) and \( u_{LW} \) are the
vectors of additive genetic sire effects, \( l \) is the vector of
common litter effect, \( d \) is the vector of parental dominance
effect, \( e \) is the vector of residual effects, and \( X, Z_{LR}, Z_{LW}, 
W, \) and \( H \) are the corresponding incidence matrices. Only
one additive genetic sire effect, either LR or LW, was
included in the statistical model for purebred records.
Covariance matrices of random effects were assumed to be
\( A \otimes G_0, I \otimes L_0, D \otimes F_0, \) and \( I \otimes R_0 \) for additive genetic,
litter, parental dominance, and residual, respectively.

Estimates for dominance variance were based on
method inverting paternal dominance relationship matrix
described by Hoeschele and VanRaden (1991). All the
analyses were carried out using EM-algorithm with
REMLF90 package (Mintzal, 1998).

**Results and Discussion**

Estimates for heritability, proportion of variance due to
common litter environment and the proportion of variance
due to parental dominance of the sow longevity related traits
(stayabilities 3 and 5, length of productive life and overall
leg action) are presented in Table 1. Estimated heritabilities
are all low, and in the same magnitude between the different
analyses. However, there is a tendency for the heritability
estimates from the simplest model, containing only additive
genetic sire as a random effect (not including sow’s
inbreeding) to be higher (0.06 – 0.12) than heritability
estimates from the more complex models, which account for
different combinations of sow’s inbreeding, common litter
environment and parental dominance effects (0.03 – 0.09).

The estimated proportions of variance due to common
litter environment varied between 0.02 and 0.14 (Table 1).
Although \( \hat{\sigma}^2 \) estimates from different statistical models in
general are all in the same magnitude, it seems that the
effect of common litter environment, sow’s inbreeding and
dominance genetic effects are confounded. In general, \( \hat{\sigma}^2 \)
estimates from AL and ALF models were lower than the
 corresponding estimates from ALFD model, especially in
crossbred population (\( \hat{\sigma}^2 \) average 0.06 in both AL and ALF
models, and 0.03 in ALFD model). Thus, these estimates
indicate that common litter environment accounts part of the
variation due to dominance genetic effects in ALFD model.

Estimated genetic correlations of same traits between
crossbred and purebred populations are presented in Table
2. In general, all the correlations were very high (all over
0.75), Large White – crossbred correlations being somewhat
higher than Landrace – crossbred correlations. There is a
tendency for the correlations to increase as more
information is accounted for in the statistical model. This
increase appears to be larger among the correlations
between Landrace and crossbred breeding values than
between Large White and crossbred. For example, the
average correlation between Landrace and crossbred
population increased from 0.89 (model A) to 0.94 (model
ALFD). The corresponding increase between Large White
and crossbred population was from 0.94 to 0.95. However,
the lowest average correlation between Large White and
crossbred population was resulted by AF model (0.92).

Substantial dominance effects (\( d^2 \) ranged between 0.03
and 0.12) was found to impact these traits. The dominance
effects of this magnitude should be accounted for in the
statistical model of routine breeding value estimations.
Possible benefits appear simply by obtaining more reliable
breeding values through more correct statistical modeling,
and by accounting for dominance effects in selection.
Moreover, the estimated genetic correlations of same traits
between purebred and crossbred populations increased by
accounting the common litter environment and parental
dominance in the statistical model. In addition to the
benefits of accounting dominance effect in the statistical
model of breeding value estimation, the potential to utilize
predicted dominance effects to make planned matings in
multiplier level also exists.
Table 1. Estimates for heritability ($h^2$), proportion of variance due to common litter environment ($l^2$) and proportion of dominance variance out of phenotypic variance ($d^2$) of leg score, stayabilities until 3rd and 5th parities (Stay3, Stay5), and length of productive life (LPL) for Finnish Landrace, Large White and Landrace x Large White populations. Estimates are obtained using five different statistical models $^1$.

<table>
<thead>
<tr>
<th></th>
<th>A$^1$</th>
<th>A,F$^1$</th>
<th>$h^2$</th>
<th>A,L$^1$</th>
<th>A,L,F$^1$</th>
<th>A,L,F,D$^1$</th>
<th>$l^2$</th>
<th>A,L$^1$</th>
<th>A,L,F$^1$</th>
<th>A,L,F,D$^1$</th>
<th>$d^2$</th>
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</thead>
<tbody>
<tr>
<td><strong>Landrace</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Leg score</td>
<td>0.06</td>
<td>0.04</td>
<td>0.04</td>
<td>0.04</td>
<td>0.04</td>
<td></td>
<td>0.10</td>
<td>0.14</td>
<td>0.09</td>
<td>0.03</td>
<td>0.03</td>
</tr>
<tr>
<td>Stay3</td>
<td>0.07</td>
<td>0.07</td>
<td>0.05</td>
<td>0.06</td>
<td>0.05</td>
<td></td>
<td>0.05</td>
<td>0.06</td>
<td>0.04</td>
<td>0.03</td>
<td>0.03</td>
</tr>
<tr>
<td>Stay5</td>
<td>0.07</td>
<td>0.04</td>
<td>0.05</td>
<td>0.04</td>
<td>0.05</td>
<td></td>
<td>0.05</td>
<td>0.06</td>
<td>0.04</td>
<td>0.04</td>
<td>0.04</td>
</tr>
<tr>
<td>LPL</td>
<td>0.09</td>
<td>0.06</td>
<td>0.07</td>
<td>0.05</td>
<td>0.07</td>
<td></td>
<td>0.05</td>
<td>0.03</td>
<td>0.02</td>
<td>0.11</td>
<td>0.10</td>
</tr>
</tbody>
</table>

| **Large White** |       |         |       |         |          |             |       |         |          |             |       |
| Leg score     | 0.09  | 0.05    | 0.06  | 0.03    | 0.06     |             | 0.11  | 0.13    | 0.10     |             | 0.03 |
| Stay3         | 0.06  | 0.03    | 0.05  | 0.03    | 0.05     |             | 0.05  | 0.07    | 0.04     |             | 0.03 |
| Stay5         | 0.07  | 0.06    | 0.05  | 0.05    | 0.05     |             | 0.05  | 0.03    | 0.04     |             | 0.04 |
| LPL           | 0.08  | 0.08    | 0.06  | 0.07    | 0.06     |             | 0.06  | 0.05    | 0.03     |             | 0.10 |

| **Crossbred**  |       |         |       |         |          |             |       |         |          |             |       |
| Leg score     | 0.12  | 0.09    | 0.08  | 0.09    | 0.08     |             | 0.08  | 0.01    | 0.05     |             | 0.09 |
| Stay3         | 0.08  | 0.07    | 0.06  | 0.06    | 0.06     |             | 0.05  | 0.07    | 0.02     |             | 0.09 |
| Stay5         | 0.08  | 0.08    | 0.06  | 0.07    | 0.06     |             | 0.05  | 0.03    | 0.03     |             | 0.09 |
| LPL           | 0.06  | 0.07    | 0.05  | 0.07    | 0.04     |             | 0.05  | 0.05    | 0.02     |             | 0.12 |

$^1$ Different combinations of additive genetic sire (A), inbreeding coefficient of sow (F), common litter environment of sow (L), and parental dominance (D) were included in the statistical models.

Table 2. Genetic correlations between the same traits (leg score, stayabilities until 3rd and 5th parity [Stay3, Stay5], and length of productive life [LPL]) of from crossbred (Landrace x Large White) or purebred populations. The estimates are obtained using five different statistical models $^1$.

<table>
<thead>
<tr>
<th></th>
<th>A</th>
<th>A+F</th>
<th>A+L</th>
<th>A+L+F</th>
<th>A+L+F+D</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Landrace</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Leg score</td>
<td>0.88</td>
<td>0.93</td>
<td>0.88</td>
<td>0.93</td>
<td>0.92</td>
</tr>
<tr>
<td>Stay3</td>
<td>0.85</td>
<td>0.76</td>
<td>0.89</td>
<td>0.90</td>
<td>0.93</td>
</tr>
<tr>
<td>Stay5</td>
<td>0.90</td>
<td>0.95</td>
<td>0.92</td>
<td>0.96</td>
<td>0.94</td>
</tr>
<tr>
<td>LPL</td>
<td>0.94</td>
<td>0.94</td>
<td>0.92</td>
<td>0.95</td>
<td>0.96</td>
</tr>
</tbody>
</table>

| **Large White** |       |       |       |        |         |
| Leg score      | 0.94  | 0.93  | 0.94  | 0.93   | 0.93    |
| Stay3          | 0.91  | 0.83  | 0.93  | 0.94   | 0.95    |
| Stay5          | 0.92  | 0.93  | 0.89  | 0.93   | 0.91    |
| LPL            | 0.99  | 0.99  | 0.98  | 0.99   | 0.99    |

$^1$ Different combinations of additive genetic sire (A), inbreeding coefficient of sow (F), common litter environment of sow (L), and parental dominance (D) were included in the statistical models.